

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/540,047
Source: Pt 1/10
Date Processed by STIC: 6/30/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

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Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/540,047

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (Sec "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.

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PCT

RAW SEQUENCE LISTING

DATE: 06/30/2005

PATENT APPLICATION: US/10/540,047

TIME: 09:05:27

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\06302005\J540047.raw

3 <110> APPLICANT: FUNDACION PARA LA INVESTIGACION CLINICA Y MOLECULAR
 4 DEL CANCER DE PULMON (LUNG CANCER CLINICAL AND MOLECULAR
 5 RESEARCH FOUNDATION)
 W--> 6 <120> TITLE OF INVENTION: "ASSAY DEVICE OF XPD/ERCC2 GENE POLYMORPHISMS FOR THE
 W--> 7 CORRECT ADMINISTRATION OF CHEMOTHERAPY IN LUNG CANCER"
 W--> 8 <130> FILE REFERENCE: PCT-152
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/540,047
 C--> 9 <141> CURRENT FILING DATE: 2005-06-22
 W--> 9 <160> NUMBER OF SEQ ID: 8

*see item 4 on
 Error summary sheet*

ERRORED SEQUENCES

E--> 10 <210> SEQ ID NO.: SEQ ID NO.: 1
 11 <211> LENGTH: 15
 E--> 12 <212> TYPE: oligonucleotide
 13 <213> ORGANISM: artificial sequence
 W--> 14 <220> FEATURE:
 W--> 15 <221> NAME/KEY: primer
 W--> 16 <223> OTHER INFORMATION:
 W--> 16 <400> SEQUENCE:
 17 acgcccacct ggcca 15
 E--> 19 <210> SEQ ID NO.: SEQ ID NO.: 2
 20 <211> LENGTH: 17
 E--> 21 <212> TYPE: oligonucleotide
 22 <213> ORGANISM: artificial sequence
 W--> 23 <220> FEATURE:
 W--> 24 <221> NAME/KEY: primer
 W--> 25 <223> OTHER INFORMATION:
 W--> 25 <400> SEQUENCE:
 26 ggcgggaaag ggactgg 17
 E--> 28 <210> SEQ ID NO.: SEQ ID NO.: 3
 29 <211> LENGTH: 19
 E--> 30 <212> TYPE: oligonucleotide
 31 <213> ORGANISM: artificial sequence
 W--> 32 <220> FEATURE:
 W--> 33 <221> NAME/KEY: primer
 34 <223> OTHER INFORMATION: TaqMan MGBTM VIC Probe
 W--> 35 <400> SEQUENCE:
 36 ccgtgctgcc cgacgaagt 19
 E--> 38 <210> SEQ ID NO.: SEQ ID NO.: 4
 39 <211> LENGTH: 19
 E--> 40 <212> TYPE: oligonucleotide

*Does Not Comply
 Corrected Diskette Needed*

*See attached
 pages for error
 explanations.*

*Suggestion: consult
 Sequence Rules
 for valid format*

replace with

SEQUENCE LISTING (do not use bold print)

10/540,047

2

LIST OF SEQUENCES

do NOT include foreign accent marks. They cannot be processed.

<110> FUNDACION PARA LA INVESTIGACION CLINICA Y MOLECULAR
DEL CANCER DE PULMON (LUNG CANCER CLINICAL AND MOLECULAR
RESEARCH FOUNDATION)

<120> "ASSAY DEVICE OF XPD/ERCC2 GENE POLYMORPHISMS FOR THE
CORRECT ADMINISTRATION OF CHEMOTHERAPY IN LUNG CANCER"

<130> PCT-152

<160> 8

<210> SEQ ID NO. 1

<211> 15

<212> oligonucleotide

<213> artificial sequence

<220>

<223> primer

<400> 1< insert

acgccacacct ggcca

<210> SEQ ID NO. 2

<211> 17

<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer

<400> 2<

ggcgggaaag ggactgg

<210> SEQ ID NO. 3

<211> 19

<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer

<223> (TaqMan MGBTM VIC Probe

do NOT use ITALICS.

Use a fixed-width font, per 1.824 of Sequence Rules

invited response.
The only valid responses are: DNA, RNA, or PRT. For a combined DNA/RNA sequence, use <2127 DNA and explain in <2207-2237 section.

17

replace with
↓

explanation for Artificial Sequence goes on <2237 line

move up
↓
delete

<400> 3 ←
ccgtgctgcc cgacgaagt

19

<210> ~~SEQ ID NO.~~ 4

<211> 19

<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer

<223> TaqMan MGBTM 6-FAM Probe

<400> 4 ←

cccgtgctgc ccaacgaag

19

<210> ~~SEQ ID NO.~~ 5

<211> 22

<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer

<400> 5 ←

gcctggagca gctagaatca ga

22

<210> ~~SEQ ID NO.~~ 6

<211> 22

<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer

<400> 6 ←

cactcagagc tgctgagcaa tc

22

<210> ~~SEQ ID NO.~~ 7

<211> 16

<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer

<223> TaqMan MGBTM VIC Probe

<400> 7C

tatcctctgc agcgtc

16

<210> SEQ ID NO. 8

<211> 17

<212> oligonucleotide

<213> artificial sequence

<220>

<223> primer

<223> TaqMan MGBTM 6-FAM Probe

<400> 8C

ctatcctctt cagcgtc

17